NO NEW MATTER

The above amendments to the specification and claims introduce no new matter. In particular, the amendment to the abstract page simply removes the duplicate title of the invention; the amendments to the specification simply re-write browser executable hyperlinks to be non-executable, or correct spelling errors and the amendments to the claims merely clarify the language of the claims. Support for the claim amendments is replete throughout the specification and claims as filed.

REMARKS

STATUS OF THE APPLICATION.

Claims 43-53 are pending with entry of this amendment. The claims were previously rejected for various lack of clarity issues under 35 U.S.C. § 112, second paragraph and for alleged obviousness over Zhao et al. The rejections are believed to be overcome by the amendments to the claims; to the extent that the rejections may be applied to the amended claims, Applicants traverse for the reasons noted below.

The specification was also objected to for the inclusion of browser executable hyperlinks. As noted below, the relevant internet citations have been amended to make the citations non-executable.

OBJECTION TO THE SPECIFICATION

The specification was objected to for the inclusion of citations which included browser executable code in the text. Passages with such executable codes have been re-written to make the citations non-browser executable, i.e., by specifying addresses on the world-wide web without the prefixes "http" or "www." Accordingly, the objection should be withdrawn.

AS AMENDED THE CLAIMS ARE DEFINITE

Claims 43-53 were rejected for improper antecedence in claims 50-53 and for not more clearly relating the preamble of claim 43 with the final method step. The claims have been amended for clarity, overcoming the rejection. That is, the preamble of claim 43 is now more specifically tied into the final method step and the antecedence errors helpfully noted by the Examiner have been corrected in claims 50-53.

THE CLAIMS ARE NOT OBVIOUS OVER ZHAO

Claims 43-53 were rejected under 35 U.S.C. §103(a) as allegedly obvious in light of Zhao et al., Nature Biotechnology 16:258-261. To the extent that the rejection may be applied to the amended claims, Applicants traverse.

Claim 43 is directed towards specific methods of recombining character strings, i.e., representations of polynucleotides or polypeptides. Zhao is directed towards the recombination of nucleic acids *per se*, rather than to the recombination of such representational character strings. Applicants have amended claim 43 to make this distinction as clear as possible, as discussed with the Examiner in the helpful interview of August 8, 2001.

Because Zhao does not provide any of the limitations of the amended claims, it cannot serve as a basis for establishing a *prima facie* case of obviousness. Accordingly, Applicants respectfully ask that the rejection be withdrawn.

CONCLUSION

In view of the foregoing, Applicants believes all claims now pending in this application are in condition for allowance. The issuance of a formal Notice of Allowance at an early date is respectfully requested. **IN THE EVENT THAT ANY ISSUES REMAIN, APPLICANTS RESPECTFULLY REQUEST A TELEPHONIC EXAMINER'S INTERVIEW, PRIOR TO ISSUANCE OF ANY ADDITIONAL ACTION BY THE OFFICE.** Further, if a telephone conference would expedite prosecution of this application in any way, the Examiner is invited to telephone the undersigned at (510) 337-7871.

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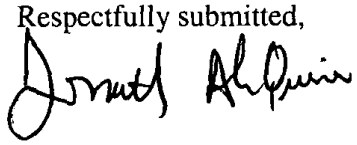
Respectfully submitted,



Jonathan Alan Quine
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APPENDIX A

"MARKED UP" CLAIMS ILLUSTRATING THE AMENDMENTS MADE TO THE CLAIMS OF 09/494,282 WITH ENTRY OF THIS AMENDMENT

43 (AMENDED). A method of making a set of derivatives of a parental character string[s], the method comprising:

a) providing [a] the parental character string, encoding a polynucleotide or polypeptide, which parental character string is a representation of the polynucleotide or polypeptide;

b) providing a set of oligonucleotide or peptide character strings of a pre-selected length that encode a plurality of single-stranded oligonucleotide or peptide subsequences of the parental character string or a complement thereof, wherein the oligonucleotide or peptide character strings are representations of oligonucleotides or peptides;

c) creating [a] the set of derivatives of the parental character string, wherein the derivatives comprise sequence variant strings each having at least one mutation as compared to the parental character string, the set comprising a plurality of mutations.

44 (AMENDED). The method of claim 43, wherein a plurality of the peptide or single-stranded oligonucleotide sequences are overlapping in sequence.

45 (AMENDED). The method of claim 43, further comprising applying one or more genetic operator to the parental character string, or to one or more of the oligonucleotide or peptide character strings, wherein the genetic operator is selected from:

a mutation of the parental character string or of one or more of the oligonucleotide or peptide character strings, a multiplication of the parental character string or of one or more of the oligonucleotide or peptide character strings[,];

a fragmentation of the parental character string or of one or more of the oligonucleotide or peptide character strings[,];

a crossover between [any of] the parental character string [or one or more of the oligonucleotide or peptide character strings, or] and an additional character string, or between one or more of the oligonucleotide or peptide character strings, or between one or more of the oligonucleotide or peptide character strings and the parental character string, or between one or more of the oligonucleotide or peptide character strings and an additional character string;

a ligation of the parental character string with an additional character string;

a ligation of one or more of the oligonucleotide or peptide character strings with one or more additional character string;

a ligation of a plurality of the oligonucleotide or peptide character strings;

a ligation of one or more of the oligonucleotide or peptide character strings with the parental character string;

an elitism calculation[,];

a calculation of sequence homology or sequence similarity of an alignment comprising the parental character string or of one or more of the oligonucleotide or peptide character strings[,];

a recursive use of one or more genetic operator for evolution of any of the character strings[,];

application of a randomness operator to the parental character string, or to one or more of the oligonucleotide or peptide character strings[,];

a deletion mutation of the parental character string, or one or more of the oligonucleotide or peptide character strings[,];

an insertion mutation into the parental character string, or into one or more of the oligonucleotide or peptide character strings[,];

subtraction of the parental character string, or of one or more of the oligonucleotide or peptide character strings, with an inactive sequence[,];

selection of the parental character string, or of one or more of the oligonucleotide or peptide character strings, with an active sequence[,]; and,

death of the parental character string, or one or more of the oligonucleotide or peptide character strings.

49 (AMENDED). The method of claim 47, further comprising:

g) selecting or screening the library for one or more recombinant polynucleotide or polypeptide having a desired property.

50 (AMENDED). The method of claim [48] 49, further comprising:

h) deconvoluting the sequence of the one or more selected polynucleotide or polypeptide.

51 (AMENDED). The method of claim [48] 50, wherein the sequence of the one or more selected polynucleotide is deconvoluted by sequencing the selected polynucleotide, or by digesting the one or more selected polynucleotide.

52 (AMENDED). The method of claim [48] 50, wherein the sequence is deconvoluted by positional deconvolution of the one or more selected polynucleotide.

53 (AMENDED). The method of claim [48] 47, further comprising reiterative shuffling or selection of the library of recombinant nucleic acids.

APPENDIX B

CLAIMS PENDING IN USSN 09/494,282 WITH ENTRY OF THIS AMENDMENT

43 (AMENDED). A method of making a set of derivatives of a parental character string, the method comprising:

a) providing the parental character string, encoding a polynucleotide or polypeptide, which parental character string is a representation of the polynucleotide or polypeptide;

b) providing a set of oligonucleotide or peptide character strings of a pre-selected length that encode a plurality of single-stranded oligonucleotide or peptide subsequences of the parental character string or a complement thereof, wherein the oligonucleotide or peptide character strings are representations of oligonucleotides or peptides;

c) creating the set of derivatives of the parental character string, wherein the derivatives comprise sequence variant strings each having at least one mutation as compared to the parental character string, the set comprising a plurality of mutations.

44 (AMENDED). The method of claim 43, wherein a plurality of the peptide or single-stranded oligonucleotide sequences are overlapping in sequence.

45 (AMENDED). The method of claim 43, further comprising applying one or more genetic operator to the parental character string, or to one or more of the oligonucleotide or peptide character strings, wherein the genetic operator is selected from:

a mutation of the parental character string or of one or more of the oligonucleotide or peptide character strings, a multiplication of the parental character string or of one or more of the oligonucleotide or peptide character strings;

a fragmentation of the parental character string or of one or more of the oligonucleotide or peptide character strings;

a crossover between the parental character string and an additional character string, or between one or more of the oligonucleotide or peptide character strings, or between one or more of the oligonucleotide or peptide character strings and the parental character string, or between one or more of the oligonucleotide or peptide character strings and an additional character string;

a ligation of the parental character string with an additional character string;

a ligation of one or more of the oligonucleotide or peptide character strings with one or more additional character string;

a ligation of a plurality of the oligonucleotide or peptide character strings;

a ligation of one or more of the oligonucleotide or peptide character strings with the parental character string;

an elitism calculation;

a calculation of sequence homology or sequence similarity of an alignment comprising the parental character string or of one or more of the oligonucleotide or peptide character strings;

a recursive use of one or more genetic operator for evolution of any of the character strings;

application of a randomness operator to the parental character string, or to one or more of the oligonucleotide or peptide character strings;

a deletion mutation of the parental character string, or one or more of the oligonucleotide or peptide character strings;

an insertion mutation into the parental character string, or into one or more of the oligonucleotide or peptide character strings;

subtraction of the parental character string, or of one or more of the oligonucleotide or peptide character strings, with an inactive sequence;

selection of the parental character string, or of one or more of the oligonucleotide or peptide character strings, with an active sequence; and,

death of the parental character string, or one or more of the oligonucleotide or peptide character strings.

46. The method of claim 43, further comprising:

d) providing a set of overlapping character strings of a pre-defined length that encode both strands of the parental character string; and,

e) synthesizing sets of single-stranded oligonucleotides according to the step (c) and (d).

47. The method of claim 46, further comprising:

f) assembling a library of recombinant nucleic acids by assembly PCR from the single-stranded oligonucleotides.

48. A library made by the method of claim 47.

49 (AMENDED). The method of claim 47, further comprising:

g) selecting or screening the library for one or more recombinant polynucleotide or polypeptide having a desired property.

50 (AMENDED). The method of claim 49, further comprising:

h) deconvoluting the sequence of the one or more selected polynucleotide or polypeptide.

51 (AMENDED). The method of claim 50, wherein the sequence of the one or more selected polynucleotide is deconvoluted by sequencing the selected polynucleotide, or by digesting the one or more selected polynucleotide.

52 (AMENDED). The method of claim 50, wherein the sequence is deconvoluted by positional deconvolution of the one or more selected polynucleotide.

53 (AMENDED). The method of claim 47, further comprising reiterative shuffling or selection of the library of recombinant nucleic acids.

APPENDIX C

"MARKED UP" PARAGRAPHS ILLUSTRATING THE AMENDMENTS MADE TO THE SPECIFICATION OF 09/494,282 WITH ENTRY OF THIS AMENDMENT

Please delete the paragraph beginning at page 8, line 19 and ending at page 8, line 27 and substitute therefor the following new paragraph:

An introduction to genetic algorithms can be found in David E. Goldberg (1989) Genetic Algorithms in Search, Optimization and Machine Learning Addison-Wesley Pub Co; ISBN: 0201157675 and in Timothy Masters (1993) Practical Neural Network Recipes in C++ (Book&Disk edition) Academic Pr; ISBN: 0124790402. A variety of more recent references discuss the use of genetic algorithms used to solve a variety of such difficult programming problems. *See*, e.g., **[http://garage.cse.msu.edu/papers/papers-index.html] garage.cse.msu.edu/papers/papers-index.html (on the world wide web)** and the references cited therein; **[http://gaslab.cs.unr.edu/] gaslab.cs.unr.edu/ (on the world wide web)** and the references cited therein; **[http://www.aic.nrl.navy.mil/] aic.nrl.navy.mil/ (on the world wide web)** and the references cited therein; **[http://www.cs.gmu.edu/research/gag/] cs.gmu.edu/research/gag/ (on the world wide web)** and the references cited therein and **[http://www.cs.gmu.edu/research/gag/pubs.html] cs.gmu.edu/research/gag/pubs.html (on the world wide web)** and the references cited therein.

Please delete the paragraph beginning at page 16, line 7 and ending at page 16, line 30 and substitute therefor the following new paragraph:

One example algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul *et al., J. Mol. Biol.* 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information **[(http://www.ncbi.nlm.nih.gov/)] on the world-wide web at ncbi.nlm.nih.gov/**. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs

containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915).

Please delete the paragraph beginning at page 19, line 21 and ending at page 20, line 2 and substitute therefor the following new paragraph:

For example, oligonucleotides *e.g.*, for use in *in vitro* amplification/ gene reconstruction methods, for use as gene probes, or as shuffling targets (e.g., synthetic genes or gene segments) are typically synthesized chemically according to the solid phase phosphoramidite triester method described by Beaucage and Caruthers (1981), *Tetrahedron Letts.*, 22(20):1859-1862, *e.g.*, using an automated synthesizer, as described in Needham-VanDevanter *et al.* (1984) *Nucleic Acids Res.*, 12:6159-6168. Oligonucleotides can also be custom made and ordered from a variety of commercial sources known to persons of skill. There are many commercial providers of oligo synthesis services, and thus this is a broadly accessible technology. Any nucleic acid can be custom ordered from any of a variety of commercial sources, such as The Midland Certified Reagent Company (mcrc@oligos.com), The Great American Gene Company **[(http://www.genco.com)]** **(on the world-wide web at genco.com)**, ExpressGen Inc. **[(www.expressgen.com)]** **(on the world-wide web at expressgen.com)**, Operon Technologies Inc. (Alameda, CA) and many others. Similarly, peptides and antibodies can be custom ordered from any of a variety of sources, such as PeptidoGenic (pkim@ccnet.com), HTI Bio-products, inc. **[(http://www.htibio.com)]** **(on the world-wide web at htibio.com)**, BMA Biomedicals Ltd (U.K.), Bio·Synthesis, Inc., and many others.

Please delete the paragraph beginning at page 39, line 29 and ending at page 40, line 8 and substitute therefor the following new paragraph:

If the assay conditions are then altered in only one parameter, different individuals from the library will be identified as the best performers. Because the screening conditions are very similar, most amino acids are conserved between the two sets of best performers. Comparisons of the sequences (e.g., in silico) of the best enzymes under the two different conditions identifies the sequence differences responsible for the differences in performance. Principal component analysis is a powerful tool to use for identifying sequences conferring a particular property. For example, Partek Incorporated (St. Peters, Missouri; **[www.partek.com] on the world-wide web at partel.com)** provides software for pattern recognition (e.g., which provide Partek Pro 2000 Pattern Recognition Software) which can be applied to genetic algorithms for multivariate data analysis, interactive visualization, variable selection, neural & statistical modeling. Relationships can be analyzed, e.g., by Principal Components Analysis (PCA) mapped scatterplots and biplots, Multi-Dimensional Scaling (MDS) mapped scatterplots, Star plots, etc.

Please delete the paragraph beginning at page 42, line 4 and ending at page 42, line 13 and substitute therefor the following new paragraph:

For example, neural net approaches can be coupled to genetic algorithm-type programming. for example, NNUGA (Neural Network Using Genetic Algorithms) is an available program **[(http://www.cs.bgu.ac.il/~omri/NNUGA/)] (found on the world-wide web at cs.bgu.ac.il/~omri/NNUGA/)** which couples neural networks and genetic algorithms. An introduction to neural networks can be found, e.g., in Kevin Gurney (1999) An Introduction to Neural Networks, UCL Press, 1 Gunpowder Square, London EC4A 3DE, UK. and **[at http://www.shef.ac.uk/psychology/gurney/notes/index.html] on the world wide web at shef.ac.uk/psychology/gurney/notes/index.html**. Additional useful neural network references include those noted above in regard to genetic algorithms and, e.g., Christopher M. Bishop (1995) Neural Networks for Pattern Recognition Oxford Univ Press; ISBN: 0198538642; Brian D. Ripley, N. L. Hjort (Contributor) (1995) Pattern Recognition and Neural Networks Cambridge Univ Pr (Short); ISBN: 0521460867.

Please delete the paragraph beginning at page 42, line 15 and ending at page 43, line 13 and substitute therefor the following new paragraph:

A 'protein design cycle', involving cycling between theory and experiment, has led to recent advances in rational protein design. A reductionist approach, in which protein positions are classified by their local environments, has aided development of appropriate energy expressions. Protein design programs can be used to build or modify proteins with any selected set of design criteria. *See*, e.g., **[http://www.mayo.caltech.edu/] mayo.caltech.edu/ on the world wide web**; Gordon and Mayo (1999) "Branch-and-Terminate: A Combinatorial Optimization Algorithm for Protein Design" Structure with Folding and Design 7(9):1089-1098; Street and Mayo (1999) "Intrinsic ß-sheet Propensities Result from van der Waals Interactions Between Side Chains and the Local Backbone" Proc. Natl. Acad. Sci. USA, 96, 9074-9076; Gordon et al. (1999) "Energy Functions for Protein Design" Current Opinion in Structural Biology 9(4):509-513 Street and Mayo (1999) "Computational Protein Design" Structure with Folding and Design 7(5):R105-R109; Strop and Mayo (1999) "Rubredoxin Variant Folds Without Iron" J. Am. Chem. Soc. 121(11):2341-2345; Gordon and Mayo (1998) "Radical Performance Enhancements for Combinatorial Optimization Algorithms based on the Dead-End Elimination Theorem" J. Comp. Chem 19:1505-1514; Malakauskas and Mayo (1998) "Design, Structure, and Stability of a Hyperthermophilic Protein Variant" Nature Struct. Biol. 5:470. Street and Mayo (1998) "Pairwise Calculation of Protein Solvent-Accessible Surface Areas" Folding & Design 3: 253-258. Dahiyat and Mayo (1997) "De Novo Protein Design: Fully Automated Sequence Selection" Science 278:82-87; Dahiyat and Mayo (1997) "Probing the Role of Packing Specificity in Protein Design" Proc. Natl. Acad. Sci. USA 94:10172-10177; Dahiyat et al. (1997) "Automated Design of the Surface Positions of Protein Helices" Prot. Sci. 6:1333-1337; Dahiyat et al. (1997) "De Novo Protein Design: Towards Fully Automated Sequence Selection" J. Mol. Biol. 273:789-796; and Haney et al. (1997) "Structural basis for thermostability and identification of potential active site residues for adenylate kinases from the archaeal genus *Methanococcus*" Proteins 28(1):117-30. These design methods rely generally on energy expressions to evaluate the quality of different amino acid sequences for target protein structures. In any case, designed or modified proteins or character strings corresponding to proteins can be reverse translated and shuffled in silico and/or by physical shuffling. Thus, one aspect of the invention is the coupling of high-throughput rational design and in silico or physical shuffling and screening of genes to produce activities of interest.

Please delete the paragraph beginning at page 43, line 14 and ending at page 43, line 24 and substitute therefor the following new paragraph:

Similarly, molecular dynamic simulations such as those above and, e.g., Ornstein et al. (**on the world-wide web at [http://www.]**emsl.pnl.gov:2080/homes/tms/bms.html; Curr Opin Struct Biol (1999) 9(4):509-13) provide for "rational" enzyme redesign by biomolecular modeling & simulation to foster discovery of new enzymatic forms that would otherwise have a low probability of evolving biologically. For example, rational redesign of p450 cytochromes and alkane dehalogenase enzymes are a target of current rational design efforts. Any rationally designed protein (e.g., new p450 homologues or new alkaline dehydrogenase proteins) can be evolved by reverse translation and shuffling against either other designed proteins or against related natural homologous enzymes. Details on p450s can be found in Ortiz de Montellano (ed.) 1995, Cytochrome P450 Structure and Mechanism and Biochemistry, Second Edition Plenum Press (New York and London).

Please delete the paragraph beginning at page 57, line 22 and ending at page 58, line 6 and substitute therefor the following new paragraph:

Typically, PDA starts with a protein backbone structure and designs the amino acid sequence to modify the protein's properties, while maintaining it's three dimensional folding properties. Large numbers of sequences can be manipulated using PDA allowing for the design of protein structures (sequences, subsequences, etc.). PDA is described in a number of publications, including, e.g., Malakauskas and Mayo (1998) "Design, Structure and Stability of a Hyperthermophilic Protein Variant" Nature Struc. Biol. 5:470; Dahiyat and Mayo (1997) "De Novo Protein Design: Fully Automated Sequence Selection" Science, 278, 82-87. DeGrado, (1997) "Proteins from Scratch" Science, 278:80-81; Dahiyat, Sarisky and Mayo (1997) "De Novo Protein Design: Towards Fully Automated Sequence Selection" J. Mol. Biol. 273:789-796; Dahiyat and Mayo (1997) "Probing the Role of Packing Specificity in Protein Design" Proc. Natl. Acad. Sci. USA, 94:10172-10177; Hellinga (1997) "Rational Protein Design – Combining Theory and Experiment" Proc. Natl. Acad. Sci. USA, 94:10015-10017; Su and Mayo (1997)" Coupling Backbone Flexibility and Amino Acid Sequence Selection in Protein Design" Prot. Sci. 6:1701-1707; Dahiyat, Gordon and Mayo (1997) "Automated Design of the Surface Positions of Protein Helices" Prot. Sci., 6:1333-1337; Dahiyat and Mayo (1996) "Protein Design Automation" Prot. Sci., 5:895-903. Additional details regarding PDA are available from Xencor (Pasadena, California; **on the world-wide web at** [http://www.]xencor.com/).

Please delete the paragraph beginning at page 62, line 1 and ending at page 62, line 12 and substitute therefor the following new paragraph:

One approach to screening diverse libraries is to use a **[massivelly]** **massively** parallel solid-phase procedure to screen cells expressing shuffled nucleic acids, e.g., which encode enzymes for enhanced activity. **[Massivelly]** **Massively** parallel solid-phase screening apparatus using absorption, fluorescence, or FRET are available. *See*, e.g., United States Patent 5,914,245 to Bylina, et al. (1999); *see also*, [http://www.]kairos-scientific.com/ on the world wide web; Youvan et al. (1999) "Fluorescence Imaging Micro-Spectrophotometer (FIMS)" Biotechnology et alia<**on the world wide web at** **[www.]**et-al.com> 1:1-16; Yang et al. (1998) "High Resolution Imaging Microscope (HIRIM)" Biotechnology et alia, <**on the world wide web at** **[www.]**et-al.com> 4:1-20; and Youvan et al. (1999) "Calibration of Fluorescence Resonance Energy Transfer in Microscopy Using Genetically Engineered GFP Derivatives on Nickel Chelating Beads" posted **on the world wide web at [www.]**kairos-scientific.com. Following screening by these techniques, sequences of interest are typically isolated, optionally sequenced and the sequences used as set forth herein to design new sequences for in silico or other shuffling methods.

Please delete the paragraph beginning at page 69, line 9 and ending at page 69, line 21 and substitute therefor the following new paragraph:

Generally the charts are schematics of arrangements for components, and of process decision tree structures. It is apparent that many modifications of this particular arrangement for DEGAGGS, e.g., as set forth herein, can be developed and practiced. Certain quality control modules and links, as well as most of the generic artificial neural network learning components are omitted for clarity, but will be apparent to one of skill. The charts are in a continuous arrangement, each connectable head-to tail. Additional material and implementation of individual GO modules, and many arrangements of GOs in working sequences and trees, as used in GAGGS, are available in various software packages. Suitable references describing exemplar existing software are found, e.g., **on the world wide web at [http://www.]**aic.nrl.navy.mil/galist/ and at [http://www.]cs.purdue.edu/ coast/archive/clife/FAQ/www/Q20_2.htm. It will be apparent that many of the decision steps represented in Figs. 1-4 are performed most easily with the assistance of a computer, using one or more software program to facilitate selection/ decision processes.